

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/584,020  
Source: IFWO  
Date Processed by STIC: 3/30/07

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 03/30/2007

PATENT APPLICATION: US/10/584,020

TIME: 14:49:36

Input Set : N:\efs\03\_30\_07\10584020\_efs\20446003US1sequencelisting.txt

Output Set: N:\CRF4\03302007\J584020.raw

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4 <110> APPLICANT: Delagrave, Simon
6 <120> TITLE OF INVENTION: BIOTHERAPEUTICS, DIAGNOSTICS AND
7   RESEARCH REAGENTS
9 <130> FILE REFERENCE: 20446-003US1
11 <140> CURRENT APPLICATION NUMBER: US 10/584,020
12 <141> CURRENT FILING DATE: 2006-06-22
14 <150> PRIOR APPLICATION NUMBER: US 60/534,214
15 <151> PRIOR FILING DATE: 2004-01-05
17 <150> PRIOR APPLICATION NUMBER: US 60/554,102
18 <151> PRIOR FILING DATE: 2004-03-18
20 <160> NUMBER OF SEQ ID NOS: 38
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 354
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Synthetic hCASK-PDZopt
32 <400> SEQUENCE: 1
33 tttttatgcg gccagccgg ccggatccgg tatggatatg gaaaatgtta cccgtgttcg 60
34 tttagttcaa tttcaaaaaa ataccgatga accaatgggt attaccttga aaatgaatga 120
35 attgaatcat tgtattgttg cccgtattat gcatgggtgt atgattcatc gtcaaggtag 180
36 tttgcatgtt ggtgatgaaa ttcgtgaaat taatggtatt tctgttgcca atcaaacctg 240
37 tgaacaattg caaaaaatgt tgcgtgaaat gcgtgggttct attaccttta aaattgttcc 300
38 atcttatcgt acccaatctt cttctggaat tcatgcggcc gctgggtgctc cagt      354
40 <210> SEQ ID NO: 2
41 <211> LENGTH: 99
42 <212> TYPE: PRT
43 <213> ORGANISM: Artificial Sequence
45 <220> FEATURE:
46 <223> OTHER INFORMATION: Synthetic hCASK-PDZopt
48 <400> SEQUENCE: 2
49 Gly Met Asp Met Glu Asn Val Thr Arg Val Arg Leu Val Gln Phe Gln
50 1          5          10          15
51 Lys Asn Thr Asp Glu Pro Met Gly Ile Thr Leu Lys Met Asn Glu Leu
52          20          25          30
53 Asn His Cys Ile Val Ala Arg Ile Met His Gly Gly Met Ile His Arg
54          35          40          45
55 Gln Gly Thr Leu His Val Gly Asp Glu Ile Arg Glu Ile Asn Gly Ile
56          50          55          60
57 Ser Val Ala Asn Gln Thr Val Glu Gln Leu Gln Lys Met Leu Arg Glu
58 65          70          75          80
59 Met Arg Gly Ser Ile Thr Phe Lys Ile Val Pro Ser Tyr Arg Thr Gln

```

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60                               85                               90                               95
61 Ser Ser Ser
65 <210> SEQ ID NO: 3
66 <211> LENGTH: 337
67 <212> TYPE: PRT
68 <213> ORGANISM: Artificial Sequence
70 <220> FEATURE:
71 <223> OTHER INFORMATION: hCASK-PDZ-GST fusion
73 <400> SEQUENCE: 3
74 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
75 1 5 10 15
76 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
77 20 25 30
78 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
79 35 40 45
80 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
81 50 55 60
82 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
83 65 70 75 80
84 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 85 90 95
86 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
87 100 105 110
88 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
89 115 120 125
90 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
91 130 135 140
92 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
93 145 150 155 160
94 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
95 165 170 175
96 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
97 180 185 190
98 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
99 195 200 205
100 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
101 210 215 220
102 Gly Ser Arg Arg Ala Ser Val Gly Ser Gly Met Asp Met Glu Asn Val
103 225 230 235 240
104 Thr Arg Val Arg Leu Val Gln Phe Gln Lys Asn Thr Asp Glu Pro Met
105 245 250 255
106 Gly Ile Thr Leu Lys Met Asn Glu Leu Asn His Cys Ile Val Ala Arg
107 260 265 270
108 Ile Met His Gly Gly Met Ile His Arg Gln Gly Thr Leu His Val Gly
109 275 280 285
110 Asp Glu Ile Arg Glu Ile Asn Gly Ile Ser Val Ala Asn Gln Thr Val
111 290 295 300
112 Glu Gln Leu Gln Lys Met Leu Arg Glu Met Arg Gly Ser Ile Thr Phe
113 305 310 315 320

```

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```

114 Lys Ile Val Pro Ser Tyr Arg Thr Gln Ser Ser Ser Gly Ile His Arg
115           325           330           335
116 Asp
120 <210> SEQ ID NO: 4
121 <211> LENGTH: 590
122 <212> TYPE: PRT
123 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: hCASK-PDZ-alkaline phosphatase fusion
128 <400> SEQUENCE: 4
129 Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
130 1           5           10           15
131 Phe Cys Leu Pro Val Phe Ala Gly Met Asp Met Glu Asn Val Thr Arg
132           20           25           30
133 Val Arg Leu Val Gln Phe Gln Lys Asn Thr Asp Glu Pro Met Gly Ile
134           35           40           45
135 Thr Leu Lys Met Asn Glu Leu Asn His Cys Ile Val Ala Arg Ile Met
136           50           55           60
137 His Gly Gly Met Ile His Arg Gln Gly Thr Leu His Val Gly Asp Glu
138 65           70           75           80
139 Ile Arg Glu Ile Asn Gly Ile Ser Val Ala Asn Gln Thr Val Glu Gln
140           85           90           95
141 Leu Gln Lys Met Leu Arg Glu Met Arg Gly Ser Ile Thr Phe Lys Ile
142           100          105          110
143 Val Pro Ser Tyr Arg Thr Gln Ser Ser Ser Arg Thr Pro Glu Met Pro
144           115          120          125
145 Leu Gln Gly Thr Ala Val Asp Gly Gly Gly Gly Ser Met His Ala Ser
146           130          135          140
147 Leu Glu Val Leu Glu Asn Arg Ala Ala Gln Gly Asp Ile Thr Ala Pro
148 145          150          155          160
149 Gly Gly Ala Arg Arg Leu Thr Gly Asp Gln Thr Ala Ala Leu Arg Asp
150           165          170          175
151 Ser Leu Ser Asp Lys Pro Ala Lys Asn Ile Ile Leu Leu Ile Gly Asp
152           180          185          190
153 Gly Met Gly Asp Ser Glu Ile Thr Ala Ala Arg Asn Tyr Ala Glu Gly
154           195          200          205
155 Ala Gly Gly Phe Phe Lys Gly Ile Asp Ala Leu Pro Leu Thr Gly Gln
156           210          215          220
157 Tyr Thr His Tyr Ala Leu Asn Lys Lys Thr Gly Lys Pro Asp Tyr Val
158 225          230          235          240
159 Thr Asp Ser Ala Ala Ser Ala Thr Ala Trp Ser Thr Gly Val Lys Thr
160           245          250          255
161 Tyr Asn Gly Ala Leu Gly Val Asp Ile His Glu Lys Asp His Pro Thr
162           260          265          270
163 Ile Leu Glu Met Ala Lys Ala Ala Gly Leu Ala Thr Gly Asn Val Ser
164           275          280          285
165 Thr Ala Glu Leu Gln Asp Ala Thr Pro Ala Ala Leu Val Ala His Val
166           290          295          300
167 Thr Ser Arg Lys Cys Tyr Gly Pro Ser Ala Thr Ser Glu Lys Cys Pro

```

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```

168 305          310          315          320
169 Gly Asn Ala Leu Glu Lys Gly Gly Lys Gly Ser Ile Thr Glu Gln Leu
170          325          330          335
171 Leu Asn Ala Arg Ala Asp Val Thr Leu Gly Gly Gly Ala Lys Thr Phe
172          340          345          350
173 Ala Glu Thr Ala Thr Ala Gly Glu Trp Gln Gly Lys Thr Leu Arg Glu
174          355          360          365
175 Gln Ala Gln Ala Arg Gly Tyr Gln Leu Val Ser Asp Ala Ala Ser Leu
176          370          375          380
177 Asn Ser Val Thr Glu Ala Asn Gln Gln Lys Pro Leu Leu Gly Leu Phe
178 385          390          395          400
179 Ala Asp Gly Asn Met Pro Val Arg Trp Leu Gly Pro Lys Ala Thr Tyr
180          405          410          415
181 His Gly Asn Ile Asp Lys Pro Ala Val Thr Cys Thr Pro Asn Pro Gln
182          420          425          430
183 Arg Asn Asp Ser Val Pro Thr Leu Ala Gln Met Thr Asp Lys Ala Ile
184          435          440          445
185 Glu Leu Leu Ser Lys Asn Glu Lys Gly Phe Phe Leu Gln Val Glu Gly
186          450          455          460
187 Ala Ser Ile Asp Lys Gln Asp His Ala Ala Asn Pro Cys Gly Gln Ile
188 465          470          475          480
189 Gly Glu Thr Val Asp Leu Asp Glu Ala Val Gln Arg Ala Leu Glu Phe
190          485          490          495
191 Ala Lys Lys Glu Gly Asn Thr Leu Val Ile Val Thr Ala Asp His Ala
192          500          505          510
193 His Ala Ser Gln Ile Val Ala Pro Asp Thr Lys Ala Pro Gly Leu Thr
194          515          520          525
195 Gln Ala Leu Asn Thr Lys Asp Gly Ala Val Met Val Met Ser Tyr Gly
196          530          535          540
197 Asn Ser Glu Glu Asp Ser Gln Glu His Thr Gly Ser Gln Leu Arg Ile
198 545          550          555          560
199 Ala Ala Tyr Gly Pro His Ala Ala Asn Val Val Gly Leu Thr Asp Gln
200          565          570          575
201 Thr Asp Leu Phe Tyr Thr Met Lys Ala Ala Leu Gly Leu Lys
202          580          585          590
205 <210> SEQ ID NO: 5
206 <211> LENGTH: 351
207 <212> TYPE: PRT
208 <213> ORGANISM: Artificial Sequence
210 <220> FEATURE:
211 <223> OTHER INFORMATION: hCASK-PDZ-fc fusion protein
213 <400> SEQUENCE: 5
214 Met Arg Ala Pro Ala Gln Ile Phe Gly Phe Leu Leu Leu Leu Phe Pro
215 1          5          10          15
216 Gly Thr Arg Cys Gly Met Asp Met Glu Asn Val Thr Arg Val Arg Leu
217          20          25          30
218 Val Gln Phe Gln Lys Asn Thr Asp Glu Pro Met Gly Ile Thr Leu Lys
219          35          40          45
220 Met Asn Glu Leu Asn His Cys Ile Val Ala Arg Ile Met His Gly Gly

```

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```

221      50                      55                      60
222 Met Ile His Arg Gln Gly Thr Leu His Val Gly Asp Glu Ile Arg Glu
223 65                      70                      75                      80
224 Ile Asn Gly Ile Ser Val Ala Asn Gln Thr Val Glu Gln Leu Gln Lys
225                      85                      90                      95
226 Met Leu Arg Glu Met Arg Gly Ser Ile Thr Phe Lys Ile Val Pro Ser
227                      100                      105                      110
228 Tyr Arg Thr Gln Ser Ser Ser Glu Pro Lys Ser Cys Asp Lys Thr His
229                      115                      120                      125
230 Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
231                      130                      135                      140
232 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
233 145                      150                      155                      160
234 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
235                      165                      170                      175
236 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
237                      180                      185                      190
238 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
239                      195                      200                      205
240 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Asp Tyr Lys
241                      210                      215                      220
242 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Met Gln Lys Thr Ile
243 225                      230                      235                      240
244 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
245                      245                      250                      255
246 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
247                      260                      265                      270
248 Val Lys Gly Phe Tyr Pro Arg His Ile Ala Val Glu Trp Glu Ser Asn
249                      275                      280                      285
250 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
251                      290                      295                      300
252 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
253 305                      310                      315                      320
254 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
255                      325                      330                      335
256 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
257                      340                      345                      350
260 <210> SEQ ID NO: 6
261 <211> LENGTH: 128
262 <212> TYPE: PRT
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: polyhistidine tagged and secreted hCASK-PDZ
268 <400> SEQUENCE: 6
269 Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
270 1      5      10      15
271 Phe Cys Leu Pro Val Phe Ala Gly Met Asp Met Glu Asn Val Thr Arg
272      20      25      30
273 Val Arg Leu Val Gln Phe Gln Lys Asn Thr Asp Glu Pro Met Gly Ile

```

## RAW SEQUENCE LISTING ERROR SUMMARY

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Input Set : N:\efs\03\_30\_07\10584020\_efs\20446003US1sequencelisting.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:16; N Pos. ~~25,26,31,32,37,38~~

Seq#:18; N Pos. 23,24,26,27,35,36

Seq#:20; N Pos. 179,180,185,186,191,192,335,336,344,345,347,348

Seq#:21; N Pos. 26

Seq#:25; N Pos. 191

## VERIFICATION SUMMARY

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Input Set : N:\efs\03\_30\_07\10584020\_efs\20446003US1sequencelisting.txt

Output Set: N:\CRF4\03302007\J584020.raw

L:530 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0  
L:557 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0  
L:586 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:120  
M:341 Repeated in SeqNo=20  
L:608 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0  
L:660 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:180